PCT09

RAW SEQUENCE LISTING   DATE: 10/30/2001
PATENT APPLICATION: US/09/889,616   TIME: 12:48:09

Input Set : N:\Crf3\RULE60\09889616.txt
Output Set: N:\CRF3\10302001\I889616.raw

```
      1 <110> APPLICANT: INCYTE PHARMACEUTICALS, INC.
      2        TANG, Y. Tom
      3        LAL, Preeti
      4        HILLMAN, Jennifer L.
      5        YUE, Henry
      6        AZIMZAI, Yalda
      7        LU, Aina M.D.
      8        BAUGHN, Mariah R.
      9        TRAN, Bao
     10        SHIH, Leo L.
     11        AU-YOUNG, Janice
W--> 12 <120> TITLE OF INVENTION: NUCLEIC ACID-BINDING PROTEINS
W--> 13 <130> FILE REFERENCE: PF-0662 PCT
     15 <140> CURRENT APPLICATION NUMBER: 09/889,616
     16 <141> CURRENT FILING DATE: 2001-07-16
     18 <150> PRIOR APPLICATION NUMBER: PCT/US00/02237
     19 <151> PRIOR FILING DATE: 2000-01-28
     21 <160> NUMBER OF SEQ ID NOS: 110
     22 <170> SOFTWARE: PERL Program
     24 <210> SEQ ID NO: 1
     25 <211> LENGTH: 754
     26 <212> TYPE: PRT
     27 <213> ORGANISM: Homo sapiens
W--> 28 <220> FEATURE:
W--> 29 <221> NAME/KEY: misc-feature
     30 <223> OTHER INFORMATION: Incyte ID No.: 025733CD1
W--> 31 <400> SEQUENCE: 1
     32        Met Ala Ala Ala Gly Ser Arg Lys Arg Arg Leu Ala Glu Leu Thr
     33          1               5                  10                  15
     34        Val Asp Glu Phe Leu Ala Ser Gly Phe Asp Ser Glu Ser Glu Ser
     35                          20                  25                  30
     36        Glu Ser Glu Asn Ser Pro Gln Ala Glu Thr Arg Glu Ala Arg Glu
     37                          35                  40                  45
     38        Ala Ala Arg Ser Pro Asp Lys Pro Gly Gly Ser Pro Ser Ala Ser
     39                          50                  55                  60
     40        Arg Arg Lys Gly Arg Ala Ser Glu His Lys Asp Gln Leu Ser Arg
     41                          65                  70                  75
     42        Leu Lys Asp Arg Asp Pro Glu Phe Tyr Lys Phe Leu Gln Glu Asn
     43                          80                  85                  90
     44        Asp Gln Ser Leu Leu Asn Phe Ser Asp Ser Asp Ser Ser Glu Glu
     45                          95                 100                 105
     46        Glu Glu Gly Pro Phe His Ser Leu Pro Asp Val Leu Glu Glu Ala
     47                         110                 115                 120
     48        Ser Glu Glu Glu Asp Gly Ala Glu Glu Gly Glu Asp Gly Asp Arg
     49                         125                 130                 135
     50        Val Pro Arg Gly Leu Lys Gly Lys Lys Asn Ser Val Pro Val Thr
     51                         140                 145                 150
```

```
52        Val Ala Met Val Glu Arg Trp Lys Gln Ala Ala Lys Gln Arg Leu
53                    155                 160                 165
54        Thr Pro Lys Leu Phe His Glu Val Val Gln Ala Phe Arg Ala Ala
55                    170                 175                 180
56        Val Ala Thr Thr Arg Gly Asp Gln Glu Ser Ala Glu Ala Asn Lys
57                    185                 190                 195
58        Phe Gln Val Thr Asp Ser Ala Ala Phe Asn Ala Leu Val Thr Phe
59                    200                 205                 210
60        Cys Ile Arg Asp Leu Ile Gly Cys Leu Gln Lys Leu Leu Phe Gly
61                    215                 220                 225
62        Lys Val Ala Lys Asp Ser Ser Arg Met Leu Gln Pro Ser Ser Ser
63                    230 .               235                 240
64        Pro Leu Trp Gly Lys Leu Arg Val Asp Ile Lys Ala Tyr Leu Gly
65                    245                 250                 255
66        Ser Ala Ile Gln Leu Val Ser Cys Leu Ser Glu Thr Thr Val Leu
67                    260                 265                 270
68        Ala Ala Val Leu Arg His Ile Ser Val Leu Val Pro Cys Phe Leu
69                    275                 280                 285
70        Thr Phe Pro Lys Gln Cys Arg Met Leu Leu Lys Arg Met Val Val
71                    290                 295                 300
72        Val Trp Ser Thr Gly Glu Glu Ser Leu Arg Val Leu Ala Phe Leu
73                    305                 310                 315
74        Val Leu Ser Arg Val Cys Arg His Lys Lys Asp Thr Phe Leu Gly
75                    320                 325                 330
76        Pro Val Leu Lys Gln Met Tyr Ile Thr Tyr Val Arg Asn Cys Lys
77                    335                 340                 345
78        Phe Thr Ser Pro Gly Ala Leu Pro Phe Ile Ser Phe Met Gln Trp
79                    350                 355                 360
80        Thr Leu Thr Glu Leu Leu Ala Leu Glu Pro Gly Val Ala Tyr Gln
81                    365                 370                 375
82        His Ala Phe Leu Tyr Ile Arg Gln Leu Ala Ile His Leu Arg Asn
83                    380                 385                 390
84        Ala Met Thr Thr Arg Lys Lys Glu Thr Tyr Gln Ser Val Tyr Asn
85                    395                 400                 405
86        Trp Gln Tyr Val His Cys Leu Phe Leu Trp Cys Arg Val Leu Ser
87                    410                 415                 420
88        Thr Ala Gly Pro Ser Glu Ala Leu Gln Pro Leu Val Tyr Pro Leu
89                    425                 430                 435
90        Ala Gln Val Ile Ile Gly Cys Ile Lys Leu Ile Pro Thr Ala Arg
91                    440                 445                 450
92        Phe Tyr Pro Leu Arg Met His Cys Ile Arg Ala Leu Thr Leu Leu
93                    455                 460                 465
94        Ser Gly Ser Ser Gly Ala Phe Ile Pro Val Leu Pro Phe Ile Leu
95                    470                 475                 480
96        Glu Met Phe Gln Gln Val Asp Phe Asn Arg Lys Pro Gly Arg Met
97                    485                 490                 495
98        Ser Ser Lys Pro Ile Asn Phe Ser Val Ile Leu Lys Leu Ser Asn
99                    500                 505                 510
100         Val Asn Leu Gln Glu Lys Ala Tyr Arg Asp Gly Leu Val Glu Gln
```

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Input Set : N:\Crf3\RULE60\09889616.txt
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```
101                      515                  520                  525
102      Leu Tyr Asp Leu Thr Leu Glu Tyr Leu His Ser Gln Ala His Cys
103                      530                  535                  540
104      Ile Gly Phe Pro Glu Leu Val Leu Pro Val Val Leu Gln Leu Lys
105                      545                  550                  555
106      Ser Phe Leu Arg Glu Cys Lys Val Ala Asn Tyr Cys Arg Gln Val
107                      560                  565                  570
108      Gln Gln Leu Leu Gly Lys Val Gln Glu Asn Ser Ala Tyr Ile Cys
109                      575                  580                  585
110      Ser Arg Arg Gln Arg Val Ser Phe Gly Val Ser Glu Gln Gln Ala
111                      590                  595                  600
112      Val Glu Ala Trp Glu Lys Leu Thr Arg Glu Glu Gly Thr Pro Leu
113                      605                  610                  615
114      Thr Leu Tyr Tyr Ser His Trp Arg Lys Leu Arg Asp Arg Glu Ile
115                      620                  625                  630
116      Gln Leu Glu Ile Ser Gly Lys Glu Arg Leu Glu Asp Leu Asn Phe
117                      635                  640                  645
118      Pro Glu Ile Lys Arg Arg Lys Met Ala Asp Arg Lys Asp Glu Asp
119                      650                  655                  660
120      Arg Lys Gln Phe Lys Asp Leu Phe Asp Leu Asn Ser Ser Glu Glu
121                      665                  670                  675
122      Asp Asp Thr Glu Gly Phe Ser Glu Arg Gly Ile Leu Arg Pro Leu
123                      680                  685                  690
124      Ser Thr Arg His Gly Val Glu Asp Asp Glu Glu Asp Glu Glu Glu
125                      695                  700                  705
126      Gly Glu Glu Asp Ser Ser Asn Ser Glu Gly Glu Trp Ser Trp Asp
127                      710                  715                  720
128      Gly Asp Pro Asp Ala Glu Ala Gly Leu Ala Pro Gly Glu Leu Gln
129                      725                  730                  735
130      Gln Leu Ala Gln Gly Pro Glu Asp Glu Leu Glu Asp Leu Gln Leu
131                      740                  745                  750
132      Ser Glu Asp Asp
134 <210> SEQ ID NO: 2
135 <211> LENGTH: 593
136 <212> TYPE: PRT
137 <213> ORGANISM: Homo sapiens
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W--> 138 <220> FEATURE:
W--> 139 <221> NAME/KEY: misc-feature
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    140 <223> OTHER INFORMATION: Incyte ID No.: 079702CD1
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W--> 141 <400> SEQUENCE: 2
```
    142      Met Arg Asp Ser Thr Gly Ala Gly Asn Ser Leu Val His Lys Arg
    143       1               5                  10                  15
    144      Ser Pro Leu Arg Arg Asn Gln Lys Thr Pro Thr Ser Leu Thr Lys
    145                       20                 25                  30
    146      Leu Ser Leu Gln Asp Gly His Lys Ala Lys Lys Pro Ala Cys Lys
    147                       35                 40                  45
    148      Phe Glu Glu Gly Gln Asp Val Leu Ala Arg Trp Ser Asp Gly Leu
    149                       50                 55                  60
    150      Phe Tyr Leu Gly Thr Ile Lys Lys Ile Asn Ile Leu Lys Gln Ser
```

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```
151                        65                    70                        75
152        Cys Phe Ile Ile Phe Glu Asp Ser Ser Lys Ser Trp Val Leu Trp
153                        80                    85                        90
154        Lys Asp Ile Gln Thr Gly Ala Thr Gly Ser Gly Glu Met Val Cys
155                        95                   100                       105
156        Thr Ile Cys Gln Glu Glu Tyr Ser Glu Ala Pro Asn Glu Met Val
157                       110                   115                       120
158        Ile Cys Asp Lys Cys Gly Gln Gly Tyr His Gln Leu Cys His Thr
159                       125                   130                       135
160        Pro His Ile Asp Ser Ser Val Ile Asp Ser Asp Glu Lys Trp Leu
161                       140                   145                       150
162        Cys Arg Gln Cys Val Phe Ala Thr Thr Thr Lys Arg Gly Gly Ala
163                       155                   160                       165
164        Leu Lys Lys Gly Pro Asn Ala Lys Ala Leu Gln Val Met Lys Gln
165                       170                   175                       180
166        Thr Leu Pro Tyr Ser Val Ala Asp Leu Glu Trp Asp Ala Gly His
167                       185                   190                       195
168        Lys Thr Asn Val Gln Gln Cys Tyr Cys Tyr Cys Gly Gly Pro Gly
169                       200                   205                       210
170        Asp Trp Tyr Leu Lys Met Leu Gln Cys Cys Lys Cys Lys Gln Trp
171                       215                   220                       225
172        Phe His Glu Ala Cys Val Gln Cys Leu Gln Lys Pro Met Leu Phe
173                       230                   235                       240
174        Gly Asp Arg Phe Tyr Thr Phe Ile Cys Ser Val Cys Ser Ser Gly
175                       245                   250                       255
176        Pro Glu Tyr Leu Lys Arg Leu Pro Leu Gln Trp Val Asp Ile Ala
177                       260                   265                       270
178        His Leu Cys Leu Tyr Asn Leu Ser Val Ile His Lys Lys Lys Tyr
179                       275                   280                       285
180        Phe Asp Ser Glu Leu Glu Leu Met Thr Tyr Ile Asn Glu Asn Trp
181                       290                   295                       300
182        Asp Arg Leu His Pro Gly Glu Leu Ala Asp Thr Pro Lys Ser Glu
183                       305                   310                       315
184        Arg Tyr Glu His Val Leu Glu Ala Leu Asn Asp Tyr Lys Thr Met
185                       320                   325                       330
186        Phe Met Ser Gly Lys Glu Ile Lys Lys Lys Lys His Leu Phe Gly
187                       335                   340                       345
188        Leu Arg Ile Arg Val Pro Pro Val Pro Pro Asn Val Ala Phe Lys
189                       350                   355                       360
190        Ala Glu Lys Glu Pro Glu Gly Thr Ser His Glu Phe Lys Ile Lys
191                       365                   370                       375
192        Gly Arg Lys Ala Ser Lys Pro Ile Ser Asp Ser Arg Glu Val Ser
193                       380                   385                       390
194        Asn Gly Ile Glu Lys Lys Lys Lys Lys Lys Ser Val Gly Arg Pro
195                       395                   400                       405
196        Pro Gly Pro Tyr Thr Arg Lys Met Ile Gln Lys Thr Ala Glu Pro
197                       410                   415                       420
198        Leu Leu Asp Lys Glu Ser Ile Ser Glu Asn Pro Thr Leu Asp Leu
199                       425                   430                       435
```

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```
200        Pro Cys Ser Ile Gly Arg Thr Glu Gly Thr Ala His Ser Ser Asn
201                    440                 445                 450
202        Thr Ser Asp Val Asp Phe Thr Gly Ala Ser Ser Ala Lys Glu Thr
203                    455                 460                 465
204        Thr Ser Ser Ser Ile Ser Arg His Tyr Gly Leu Ser Asp Ser Arg
205                    470                 475                 480
206        Lys Arg Thr Arg Thr Gly Arg Ser Trp Pro Ala Ala Ile Pro His
207                    485                 490                 495
208        Leu Arg Arg Arg Arg Gly Arg Leu Pro Arg Arg Ala Leu Gln Thr
209                    500                 505                 510
210        Gln Asn Ser Glu Ile Val Lys Asp Asp Glu Gly Lys Glu Asp Tyr
211                    515                 520                 525
212        Gln Phe Asp Glu Leu Asn Thr Glu Ile Leu Asn Asn Leu Ala Asp
213                    530                 535                 540
214        Gln Glu Leu Gln Leu Asn His Leu Lys Asn Ser Ile Thr Ser Tyr
215                    545                 550                 555
216        Phe Gly Ala Ala Gly Arg Ile Ala Cys Gly Glu Lys Tyr Arg Val
217                    560                 565                 570
218        Leu Ala Arg Arg Val Thr Leu Asp Gly Lys Val Gln Tyr Leu Val
219                    575                 580                 585
220        Glu Trp Glu Gly Ala Thr Ala Ser
221                    590
223 <210> SEQ ID NO: 3
224 <211> LENGTH: 534
225 <212> TYPE: PRT
226 <213> ORGANISM: Homo sapiens
```

W--> 227 `<220>` FEATURE:
W--> 228 `<221>` NAME/KEY: misc-feature
```
229 <223> OTHER INFORMATION: Incyte ID No.: 116208CD1
```
W--> 230 `<400>` SEQUENCE: 3
```
231        Met Arg Ala Leu His Leu Leu Lys Ser Gly Cys Ser Pro Ala Val
232          1               5                  10                  15
233        Gln Ile Lys Ile Arg Glu Leu Tyr Arg Arg Arg Tyr Pro Arg Thr
234                     20                  25                  30
235        Leu Glu Gly Leu Ser Asp Leu Ser Thr Ile Lys Ser Ser Val Phe
236                     35                  40                  45
237        Ser Leu Asp Gly Gly Ser Ser Pro Val Glu Pro Asp Leu Ala Val
238                     50                  55                  60
239        Ala Gly Ile His Ser Leu Pro Ser Thr Ser Val Thr Pro His Ser
240                     65                  70                  75
241        Pro Ser Ser Pro Val Gly Ser Val Leu Leu Gln Asp Thr Lys Pro
242                     80                  85                  90
243        Thr Phe Glu Met Gln Gln Pro Ser Pro Pro Ile Pro Pro Val His
244                     95                 100                 105
245        Pro Asp Val Gln Leu Lys Asn Leu Pro Phe Tyr Asp Val Leu Asp
246                    110                 115                 120
247        Val Leu Ile Lys Pro Thr Ser Leu Val Gln Ser Ser Ile Gln Arg
248                    125                 130                 135
249        Phe Gln Glu Lys Phe Phe Ile Phe Ala Leu Thr Pro Gln Gln Val
```

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Input Set : N:\Crf3\RULE60\09889616.txt
Output Set: N:\CRF3\10302001\I889616.raw

```
L:12 M:283 W: Missing Blank Line separator, <120> field identifier
L:13 M:283 W: Missing Blank Line separator, <130> field identifier
L:28 M:283 W: Missing Blank Line separator, <220> field identifier
L:29 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:31 M:283 W: Missing Blank Line separator, <400> field identifier
L:138 M:283 W: Missing Blank Line separator, <220> field identifier
L:139 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:141 M:283 W: Missing Blank Line separator, <400> field identifier
L:227 M:283 W: Missing Blank Line separator, <220> field identifier
L:228 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:230 M:283 W: Missing Blank Line separator, <400> field identifier
L:308 M:283 W: Missing Blank Line separator, <220> field identifier
L:309 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:311 M:283 W: Missing Blank Line separator, <400> field identifier
L:351 M:283 W: Missing Blank Line separator, <220> field identifier
L:352 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:354 M:283 W: Missing Blank Line separator, <400> field identifier
L:436 M:283 W: Missing Blank Line separator, <220> field identifier
L:437 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:439 M:283 W: Missing Blank Line separator, <400> field identifier
L:503 M:283 W: Missing Blank Line separator, <220> field identifier
L:504 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:506 M:283 W: Missing Blank Line separator, <400> field identifier
L:619 M:283 W: Missing Blank Line separator, <220> field identifier
L:620 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:622 M:283 W: Missing Blank Line separator, <400> field identifier
L:647 M:283 W: Missing Blank Line separator, <220> field identifier
L:648 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
L:650 M:283 W: Missing Blank Line separator, <400> field identifier
L:688 M:283 W: Missing Blank Line separator, <220> field identifier
L:689 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:10
L:691 M:283 W: Missing Blank Line separator, <400> field identifier
L:757 M:283 W: Missing Blank Line separator, <220> field identifier
L:758 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:11
L:760 M:283 W: Missing Blank Line separator, <400> field identifier
L:824 M:283 W: Missing Blank Line separator, <220> field identifier
L:825 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:12
L:827 M:283 W: Missing Blank Line separator, <400> field identifier
L:913 M:283 W: Missing Blank Line separator, <220> field identifier
L:914 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:13
L:916 M:283 W: Missing Blank Line separator, <400> field identifier
L:986 M:283 W: Missing Blank Line separator, <220> field identifier
L:987 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:989 M:283 W: Missing Blank Line separator, <400> field identifier
L:1053 M:283 W: Missing Blank Line separator, <220> field identifier
L:1054 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15
L:1056 M:283 W: Missing Blank Line separator, <400> field identifier
L:1106 M:283 W: Missing Blank Line separator, <220> field identifier
```

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Input Set : N:\Crf3\RULE60\09889616.txt
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```
L:1107 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16
L:1109 M:283 W: Missing Blank Line separator, <400> field identifier
L:1139 M:283 W: Missing Blank Line separator, <220> field identifier
L:1140 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17
L:1142 M:283 W: Missing Blank Line separator, <400> field identifier
L:1214 M:283 W: Missing Blank Line separator, <220> field identifier
L:1215 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18
L:1217 M:283 W: Missing Blank Line separator, <400> field identifier
L:1277 M:283 W: Missing Blank Line separator, <220> field identifier
L:1278 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19
L:1280 M:283 W: Missing Blank Line separator, <400> field identifier
L:1322 M:283 W: Missing Blank Line separator, <220> field identifier
L:1323 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:1325 M:283 W: Missing Blank Line separator, <400> field identifier
L:1352 M:283 W: Missing Blank Line separator, <220> field identifier
L:1353 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
L:1355 M:283 W: Missing Blank Line separator, <400> field identifier
L:1394 M:283 W: Missing Blank Line separator, <220> field identifier
L:1395 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:22
L:1397 M:283 W: Missing Blank Line separator, <400> field identifier
L:1469 M:283 W: Missing Blank Line separator, <220> field identifier
L:1470 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:23
L:1472 M:283 W: Missing Blank Line separator, <400> field identifier
L:1500 M:283 W: Missing Blank Line separator, <220> field identifier
L:1501 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:24
L:1503 M:283 W: Missing Blank Line separator, <400> field identifier
L:1629 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:26
L:1683 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:27
L:1720 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:28
L:1743 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:29
L:1823 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:30
L:1880 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:31
L:1931 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:32
L:1956 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:33
L:2009 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:34
L:2033 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:35
L:2070 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:36
L:2108 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:37
L:2165 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:38
L:2234 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:39
L:2301 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:40
L:2358 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:41
L:2427 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:42
L:2458 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:43
L:2497 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:44
L:2578 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:45
L:2612 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:46
L:2693 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:47
L:2730 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:48
```

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Input Set : N:\Crf3\RULE60\09889616.txt
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```
L:2763 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:49
L:2810 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:50
L:2851 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:51
L:4971 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:103
L:5004 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:104
L:5190 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:110
```